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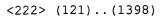
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Leu Phe Leu Lys Asp Gly Pro Tyr Gln Pro Lys Pro Ser Gln Ser Ala 165 170 Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala His Cys Ser 180 185 190 Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys Ser Leu Asp 200 Glu Thr Gly Gly Ser Phe Leu Ala Gly Ser Val Leu Ala Gly Trp Asp 215 Gly Tyr Asn Ile Thr Ser Asp Pro Asn Ala Gly Ile Gly Ser Trp Thr 230 235 Gln Gln Leu Val Gln Tyr Leu Arg Thr Gly Ser Val Pro Gly Val 245 250 Ala Gln Ala Ala Gly Pro Met Ala Glu Ala Val Glu His Ser Phe Ser 260 265 Lys Met Thr Glu Ala Asp Ile Gly Ala Ile Ala Thr Tyr Val Arg Thr 280 Val Pro Ala Val Ala Asp Ser Asn Ala Lys Gln Pro Arg Ser Ser Trp 295 300 Gly Lys Pro Ala Glu Asp Gly Leu Lys Leu Arg Gly Val Ala Leu Ala 310 315 Ser Ser Gly Ile Asp Pro Ala Arg Leu Tyr Leu Gly Asn Cys Ala Thr 325 330 Cys His Gln Met Gln Gly Lys Gly Thr Pro Asp Gly Tyr Tyr Pro Ser 345 350 340 Leu Phe His Asn Ser Thr Val Gly Ala Ser Asn Pro Ser Asn Leu Val 360 Gln Val Ile Leu Asn Gly Val Gln Arg Lys Ile Gly Ser Glu Asp Ile 375 380 Gly Met Pro Ala Phe Arg Tyr Asp Leu Asn Asp Ala Gln Ile Ala Ala 390 395 Leu Thr Asn Tyr Val Thr Ala Gln Phe Gly Asn Pro Ala Ala Lys Val 410 Thr Glu Gln Asp Val Ala Lys Leu Arg 420 <210> 17 <211> 5 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence: heme binding motif <220> <221> UNSURE <222> (2,3) <223> Xaa=unknown <400> 17

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